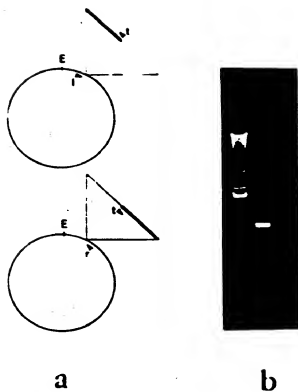


FIGURE 1

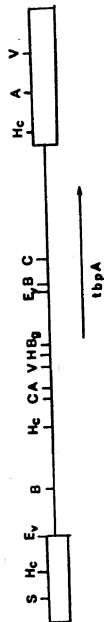


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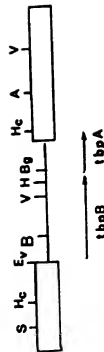
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FIGURE 2

Plasmid 9



Plasmid 10



Plasmid 482

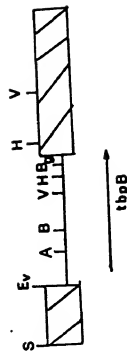


FIGURE 3

tbpB

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      10      20      30      40      50
1  CGCTTGCAG| TTTGTAAAA| ATTTAGCTAA| AATCAGACCT| GGCTTGTATT|
51 TTAGGTTTAT| TATGGAACAG| ACAACGGAAC| AAATAGATTA| TAAATTATTA|
101 AAGCATCGTT| TTCGTGGCTA| TTTACCGCIT| GTGATTGATG| TGGAACAGAG|
151 GCTTAAATGC| CCAAACCTGTG| CCTTATTGGA| ATTGGCCGGA| ATTACTTTAA|
201 AATTGGACGA| GCCAAGGTTA| TCTTATTGCC| GGATTCAACA| ATGCCAATTT|
251 CCAATTTCGG| GCCATTGGAG| GGGGCGATTT| TCAAGGGCCG| AATATTTACC|
301 CTCAGTCATT| AAAATTCAAC| GGCATTCATA| TTCACAACCC| TCTAGAGGAA|
351 GCGGTTTAGA| GAATATTGCC| CAATCCCGG| AAATGTTCAA| AATGGTTCGC|
401 AAAGCAATGA| AGGAAGCAAG| GCTGCCAACG| GGCGGTGATT| GTTGCCCCAC|
451 AATGCCACGG| TTCGATCAGG| GCTTTTTTAC| AGGCTGCGA| TTAACCGGAA|
501 TGCCAAGCGA| GAGATCCCTT| TCACCCTTTT| GGCATGTITT| GACTACCGCC|
551 GCCACCCITT| GCAGGTTTTA| TGTTATGGGC| AAACCGTGTT| CGTTAAAAGC|
601 CTGCCAGTGC| AAAATCCGTT| CACGTAGCAG| CACTATAGGG| CGAATTGGGT|
651 ACCGGGCCCC| CCTCGAGGTC| GACGGTATCG| ATAAAGCTTC| ATATCGAATT|
701 CCTGCAGCCC| GGGGGATCCG| ATGCGCCTTG| CGGCTCAAGT| TATTAGTGGC|
751 ATCGGTTTTT| TGGGTGATGG| TGTCATTTTG| CATAAGAAAA| ATGATGCGAT|
801 TTCAGGTTTA| CCCACTGCGG| CGATTATTTG| GGCTTCTGCG| GGGATCGGTA|
851 TTGCTGCAGG| GGAGGGTTTC| GTGTTTCATG| CGGTCATCGC| CACTGTCAAT|
901 ATTTTGGTGT| CTATTCGATT| ATGTCGGTTG| GTTCAACGTT| GGGTTCATCG|
951 TAAATCACAA| CGTCGTCGAC| GAAATATTCT| TGTCAATGAT| GCGGAAAGCA|
1001 TACGGAAAGT| TACCCAATTG| TTATTCAATA| ATCAGTATCG| TATTGAACAT|
1051 ATACAAGTCA| AAGATCAAAG| TAGTGGAGAA| GTTGCCGGTT| ACAAATTCGT

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FIGURE 3 CONT'D

1101 ATTGATTCCA CAATGTTCAA AGATGCGTAT GCTTTACTTA AAGCAGAAGA
1151 TGGCGAATAC TGTTCAGTA GATATCATGA AAAAGAGTGC TTATATTCAA
1201 TTTTTTATTT TTTATTTAAT TTCTTTCCAC AAAAGATCAT TTTCATTAT
1251 ATATACTGGA ATTTTGCCTT ACGCTATCTG TCATTATTATTA TGCTATTCAA
1301 GCACAACAAA CTATGGAACA ACAATCAAAA TGTACGCTTA TCGGCTGCCG
1351 ATGATTTCGA TAATGATCGA TGTGCAGAAA TATTTGAACT TACGATTTTC
1401 ACTGAGCAGT CAAAGCACGT TCGCGAGTAT CGACTCTACT TTATTTATCG
1451 TTTGTGCACT ATGTATAATC CACCTAATTC CGTGCCTTGG CCATAAAAGC
1501 CCCCTTCAA TTGTATTTAT ATCAGCTACC GTGCCACCAT TCGTACTTTT
1551 CGGATCAAGA TTAAAACAGA ATCCCTGCAT GCACAGCGAA ATCAGCTGCG
1601 GTATGCGAAA CGCCGCAGGA GCGCAGTACG CGAAGGTAC CGTCACTATC
1651 AGTGCTAGAT TTGTCAATAA AAAATTAGTG ACCAAGCTTG GGTGCATAAT
1701 GATGGTGATG AAAGAACGCT CAATGCCTGA CACGTTGCAG GCTATCTGTA
1751 AGGGTATGGT AGTTACAGGC ACAGCCCAAA CGGCCAATTG CTGGTTTTTT
1801 ATCCTTGATC CGAACAGTAC GAATGGTGGT CACGGTAGTG CATATACATA
1851 CTCAATTGAA GGGGGCTTTT ATGGCCCTAA GGCACGGAA TTAGGTGGTA
1901 TTGTACATAG TGCAGAAACG GATAAAGATA GAGTCAGTAT TACATTCGGC
1951 GGAAACGTC AAATAGAAAA ATAATCATAA TTCCCCTTTG CTGGTTGTAG
2001 ATAGCAGCGG GCAATTTTTT ATAAAAATTT GCAAAATTTA AATAA

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FIGURE 3 CONT'D

tbpA

```

      10      20      30      40      50
1  AGACCCTATC TAATGATAAT GAAATATCAT CATTTTCGCT ATTCACCTGT
51 TGCCTTAACA GTGTTATTTG CTCTTTCTCA TTCATACGGT GCTGCGACTG
101 AAAATAAAAA AATCGAAGAA AATAACGATC TAGCTGTTCT GGATGAAGTT
151 ATTGTGACAG AGAGCCATTA TGCTCACGAA CGTCAAAACG AAGTAACTGG
201 CTTGGGGAAA GTAGTGAAAA ATTATCACGA AATGAGTAAA AATCAAATTC
251 TTGGTATTCG TGATTTAACT CGCTATGACC CTGGTATTTT GGTGGTGGAA
301 CAAGGTCGCG GTGCAAGTAG TGGCTATGCC ATTGAGGTG TAGATAAAAA
351 CCGTGTCAGC TTACTTGTG ATGGGCTACC ACCAGCGCAC AGTTATCATA
401 CGCTGGTTCA GATGCTAATG GTGGTGCAAT TAATGAGATT GAGTATGAAA
451 ACATTGCTTC AATTGAGTTA AGCAAAGGAG CAAGTTCTGC GGAATATGGC
501 TCTGGTGCGC ATGGTGGTGC TATTGGTTTT CGTACTAAAG ATCGCCAGGA
551 TATTATTAAG GAGGGGCAGC ATTGGGGCTT ACATAGTAAG ACCTCTTATG
601 CCAGCAAAAA TAGCCATTTT TACAGTCTAT CGCAGCGGCT GGTGAGCGCG
651 GTGGTTTTTC AGCACTTGTT ATTGCAACTC ACCGACACGG TAAAGAGACC
701 AAAATTTCATT CCGAGGCAAA TCAATTACAT ATTATTCGGC GTATAACCGG
751 CTTTCAAAAT CGCTACGACT TTACCCAATT CCGCACAGAA TGCCTCCTGG
801 AGGATCTTTT TTTATTGTGG AAGATACTTG CCCAACATTA GATTGTACTC
851 CTCGTGCAAG GGTTAAGTTG AACGCGATAA TTTCCAGTC AGAACATTTT
901 CGAATATACG CCTGGAAGAG GCGAAACAGC TTGAGATTCC TTATCGCACT
951 GAGCTCTCAG CCCAAAGAAT ARACCGGTAA AGATCGCATT GCACCAAAAC
1001 CTTTAGATTA CAAGAGTAAT TCTGTTTTTA TGAAGTTTGG CTATCACTTT
1051 ACCTCGTCTC ATTATCTTGG CGCATCTCAC AAGATGATAC AAAACAAGCG
1101 ACGATATCCG TCATSTGCAA ACGCCAGCTT ACTATACAAA AGACGATATT
1151 TACTTATCAC TTTGGAACATA TGTTTATCAA GGGGATATTA TTTAGATGGC
1201 TTAGTGTTCA AGCCAAGGAT CCCTTATGGG TTGCGCATAT GCCATGTGAA

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FIGURE 3 CONT'D

1251 CGTCACCACA AACGTCGTTT AGGATTACACC TATAAATATA AACCAGAGAA
1301 TAATCGCTGG TTGGATAGCA TTAACGCTG CGTACGCTCT TTGGCTCTC
1351 GCTGCTGTGC TCTGAGTAAA CAAGATATTG AACTATATAG CCGGCTACAT
1401 CGCTTGCATT GTAGCGATTA TCCTGTGGTA GATAAAAATT GCGGCCCCGAC
1451 TTTGGATAAA TCTGGTCTAT GTATCGAACT GAGCGTAATA ATTACCAAGA
1501 AAAGCATCGT GTCATTCACT TAGAATTGTA TAAAGCGCTA AATGCTGGTC
1551 AAGGCGTATT TAAGCAAACC CACAACTGA ATTTAGGCTT GGGCTTTGAA
1601 TCGATTAACT GCTTATGATC ATGGGGATAT GACTGCCCAA TATACCAAG
1651 GCCGGTTATA CCAGCTACCG CGGAGAGGGG CTTTAGATAA TCCATATATT
1701 TATCGCCGCG ATCCACGCAG TATTGAAACG GTATCTTTGT GTAATAATAC
1751 AGCGGCGACA CTTAACTGTG ACGCGTTAAA TAAAGGCATA CGTTTGTACC
1801 TCGCTGCAC TTAGGAACTA TAGTTTTATG AGGGGATAAT ATTTAGATGG
1851 CTTAGTGTTT AAGCAAGCAA GGATCCCCTA TGGGTGTGCG GATATGCCAT
1901 GTGAAGTTTT TGATGAACGT CACCACAAAC GTCGTTTAGG ATTCACACCT
1951 ATAAATATAT AAACCAGAGA ATAATCGCTG GTTGATAGC ATTAACCTGT
2001 GCGTACGTGC TTTGCGCTCT CGCTGCTGTG CTGTGAGTTA AACAGATAT
2051 TGAAACTTAT AGCCGGCTAC ATCGCTTGCA TTGTGAGCGA TTATCCTGTG
2101 GTAGTAGTAA AAATTGCGGC CCGACTTTGG ATAAATCTTG GTCTATGTAT
2151 CGAACTGAGC GTAATAATTA CCAAGAAAAG CATCGTGTCA TTCATTTAGA
2201 ATTTGATAAA GCGCTAAATG CTGGTCAAGG CGTATTTAAG CAAACCCACA
2251 AACTGAATTT AGGATTGGGC TTTGAATCGA TTAATTCGCT TATGGATCAT
2301 GGGGATATGA CTGCCCAATA TACCAAAGGC CGGTTATACC AGCTAACCGC
2351 GAGAGGGCGT TTAGATAATC CATATTTATC GCCGCGATCC ACGCAGTATT
2401 GAAACGGTAT CTTTGTGTAA TAATACACGC GCGACACTAA CTGTGACGGC
2451 TTAAATAAAG GCATACGTTT GTACCTCCGC TGCTGCCTAA TAAATCAAAA
2501 GAATAACCGA GATACGGTTC AGTGTTGTTC CAACCAAGTTG CGATGGCCCA

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FIGURE 3 CONT'D

2551 CTACGTGAAC CATCACCCTA ATCAAGTTTT TTGGGGTCGA GGTGCCGTAA
2601 AGCACTTAAC CCTTCTGTCG TCTCCCGTGG ATGCTTAAAT TCGCAGCTAG

2651 TGGCAGGCAG GCACGTCCTT CCTCTCGGTG ATTTCAGGTG CAACTGACCG
2701 GTTCTTGTA CCACCCTTGA TATTAACCGG AGTCAATTAT AAAAACGAGT
2751 TACGTGGAGC GCAATTTATA ATGTCGATGT CAGATACTGT AAAACTCTAT
2801 ATTACCGTGG GCAGCAATTA GGTGACAGGG CCACGGGGCA AGCGAAACCA
2851 GACGGGTACC AATTACACCG ATTTGCCGCC CCCGGGAGAG AAATTTTCAGT
2901 TACCATTCAA AGAAGTTTAG AGCCGGCCAA AAGAAAATAC AAAAAACGCT
2951 GAAAGTATAT TCAGCGCGTT TTTGTTGCTC TAACGGATTA CATACGAATT
3001 CAAAATGTTT TAACGGTCGG TTA

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FIGURE 4

PTTBPB

.....
CGCTTGCAGATTGTAATAAATTAGCTAATAATCAGACCTGGCTGTATTTTAGCGTTATTAATG
----- Met
-10

-35

NGTBPB

.....
TTTAAATAATTAATAATATATATCTTATCATCTTTAATTGAATCGGTTTCTTTATG
----- Met
-10

-35

NMTBPB

.....
GTATTTCGAATTTTAAATAATTAATAATATATATGCTTATCATCTTTAAT TGAATTCGGTTTATAG
----- Met
-10

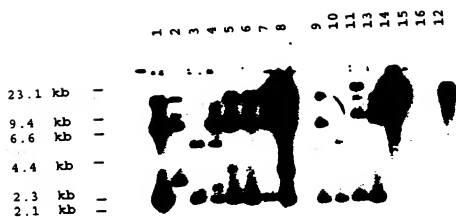
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FIGURE 5



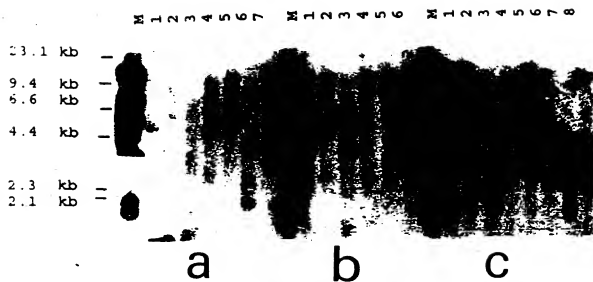
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FIGURE 6

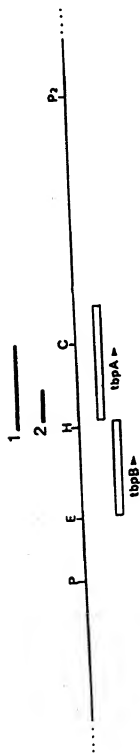
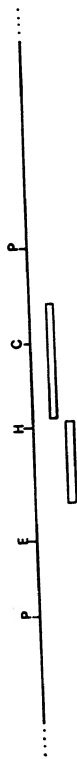


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FIGURE 7



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FIGURE 8*P. haemolytica* A1*A. suis* 3714*A. pleuropneumoniae* CMS, Shope 4074

2 kb

FIGURE 9

PHTBP	MIMKYHFRYSTVALTVLPALSHSYGAATENKKIENNDLAVLDEVITE	50
NGTBP1	MOQQ-HLFRNLILCLSLMTALP-AYAENVQAGQAQ8KQ----	44
NM1	MOQQ-HLFRNLILCLSLMTALP-VYAENVQAEQAQ8KQ----	44
PHTBP	SHYAHERQNEVTGLGKVVKVNYHEMSKNQILGIRDLTRYPGSI	100
NGTBP1	KKQKTRDRNEVTGLGKLVKTADTLSEQVLDIRDLTRYPGIAVVEQGRG	94
NM1	KKQKTRDRNEVTGLGKLVKSSDTLSKEQVLNIRDLTRYPGIAVVEQGRG	94
PHTBP	ASSGYAIRGVDKNRVSLLDVGLPQAHSYHT---LSGD---ANGGAINIEIE	144
NGTBP1	ASSGYSIRGMDKNRVSLTVDGLAQIQSYTAQAALGGTRTAGSSGAINIEIE	144
NM1	ASSGYSIRGMDKNRVSLTVDGVSQIQSYTAQAALGGTRTAGSSGAINIEIE	144
PHTBP	YENIRSIELSKGASSARYGSGAHGGAIGFRITKDAQDIIKEBQHWGLDSKT	194
NGTBP1	YENVKAVEISKGSNSVEQGGSGALAGSVAFQTKTADDVIGEGRQWGIQSKT	194
NM1	YENVKAVEISKGSNSSEYNGALAGSVAFQTKTAAIDIIGEGKQWGIQSKT	194
PHTBP	SYASKNSHFLO-IAAAGEAGCPREALVIATHRRHKETKIHSEANKLKHNR	243
NGTBP1	AYSQKNRGLTQSIAGLAGRIGGAEALLIRTGRHAGEIRAHBAAGRGVQSPN	244
NM1	AYSQKDHALTQSLALAGRSQGAELIYTKRRGREIHAHDKAGKVQSPN	244
PHTBP	RITGFENRYDFTQIPIHRMPPGGS-----FFIVEDTCPTLDCTPRARVLNRD	290
NGTBP1	RLAPVDD-----GSKYAYFIVBERECNGGHE-KCKANPKKD	279
NM1	RLVLDEDKKE-----GGSQYRYFIVBERECNG-YA-ACKNKLKED	282
PHTBP	NFPVRTFPPEYTPBERNABQIPYRTEQLSAQ8KTKGKDIRIAPNPLDYKSNSV	340
NGTBP1	VV-----GEDKRGQ-----VSTRDYTGPNRFLADPLSYESRSW	312
NM1	AS-----VKDERKT-----VSTQDYTGSNRLLANPLEYGSQSW	315
PHTBP	FMKPGYHFNSS-HYLGAILEDTKQR-TISVICRQLTIQKILTYHLGTM	388
NGTBP1	LFRPGFRFENKRHYIGILERTQQTFTDRMTVPAFLTKAVFDANQKQAG	362
NM1	LFRPGWHLDN-RHYVGAVLERTQQTFTDRMTVPAYFTSEDVVP-----G	359
PHTBP	FMKGIIFRNLVSQAK-DPLNVAHMPCEV-----DERHHKRRIGF	426
NGTBP1	SLRGNGNHKYAGNHKYGGLPTSGENNAVPGAERYGTGVFFYDETHIKSRYGL	412
NM1	SLKGLG--KYSQDNKAERLFOVQGBGSTLQCGIGYGTGVFFYDERHTIKRNVG	407
PHTBP	TYKY-KPENNRWLDINSVCRALRSCCALSQKDIELYSRLRHLCSDYP	475
NGTBP1	EYVYTNADKDTWAD---YARL-----SYDRQGIGLDNHFPQTHCSA-D	451
NM1	EYVYHNADKDTWAD---YARL-----SYDRQGIIDLNRLLQQTHCSH-D	446
PHTBP	VVDKNCQPTLDSKWSMYRTERNNYOEKHRVHLEFDLALNAGQGVFLQTH	525
NGTBP1	GSDKYCRPSADKPPSYKSDRVIYGESHKLLQAAFKKSPDTAK-----IRH	497
NM1	GSDKNCRPDGNKPPSYKSDRMIEBESRNLQAVFKKAFDTAK-----IRH	492
PHTBP	KLNLGLGPESINSLMDHGDMTAQYTLGRLYQL---PRRDPRIWTVSLCN	572
NGTBP1	NLSVNLGYDRFGSNLHQDYQYQSAN-RAYSLKTPQNNNGKTSPNGREK	546
NM1	NLSINLGYDRFQSKQLSHSDYLLQNAV-QAYDLITPK-----KPPPPNGSKD	537

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FIGURE 9 CONT'D

PHTBP	NT-----RATLNC DAL-NLGIRLYLRCLLINQLNNPRYGSVLPQPGTRV	615
NGTBP1	NPVWVSIGRGVNVTRQICLPGNNYTDCTFRSINGKSYAAV--RDNVRL	594
NM1	NPYRVSIGKTTVNTSPICRFGNNYTDCTPRNIGGNGYAAV--QDNVRL	585
	*.	
PHTBP	HRTWTPTSLGELPSIRAMAHYVNHHPNQVFWGRGAVKHLT-----LLSS	659
NGTBP1	GR-WADVGAG----LRY--DYRSTHSDGVSSTGTHRTLWNAGIVLKP	637
NM1	GR-WADVGAG----IRY--DYRSTHSEDKSVSTGTHRNLSWAGVVLKPF	628
	*.	
PHTBP	PWM-LKFAAG--RHVTL SVISG-ATDRPLVPPLILTG VNYKNES---YV	702
NGTBP1	DWLDLT YRTSTGFRLPSPFAEMYGWRSGDKIKAVKIDPEKSPNKAGIVFK	687
NM1	TWMDLT YRASTGFRLPSPFAEMYGWRAGBSLKTLDLKPEKSPNREAGIVFK	678
	*.	
PHTBP	SAIYNVDVRYCKTLY-----YRQQLGDRATGQAKPDGY--QLHRFA	742
NGTBP1	GDPGNLEASWFNNAYRDLIVRGYEAQIKDGKEQVKGNF-AYLNAQSARIT	736
NM1	GDPGNLEAS YFNNAYRDLIAPGYETRTQNGQTSASGDP-GYRNAQNARIA	727
	*.	
PHTBP	APQ-----RNPSYHKKFRPAK---ENTKNAESIFS	770
NGTBP1	GINILGKIDWNGVWDKLPBGWYSTPAYNRVRVDIKKRADRTDIQSHLFD	786
NM1	GINILGKIDWHGVWGGLPDGLYSTLAYNRIVKADIRADRTFVTSYLPD	777
	*.	
PHTBP	A-----FFVGSNGLHTNSKSCFNGRLHEPIPYFFNPLRNVPFRNEYHCCC	815
NGTBP1	AIQPSRYVVGSGYDQPEGKMGVNGMLT-----YSKAKEITELGSR---	827
NM1	AVQPSRYVLGLGYDHPDGIWINTMFT-----YSKAKSVDELLGSQ---	818
	*.	
PHTBP	TSLIAASILLHHIYHWVDFRYYYFV--YPCWILHHLIHINSFLMLLSHY	863
NGTBP1	-ALLNGNSRNTKATARRTRFWYIVDVSGYYIVKQHFTLRAGVYNLLNHRY	876
NM1	-ALLNGNANAKKAASRRTRFWYIVDVSGYYNIKKHLTLRAGVYNLLNRY	867
	*.	
PHTBP	--REVVYLTCACAFNIVTVNGF----CVGCCSNILAE MKF	898
NGTBP1	VTWENVRQTAAGAVNQHKVGVYVNRYAAPGRNYTFSLEMKF	917
NM1	VTWENVRQTAGGAVNQHKVGVYVNRYAAPGRNYTFSLEMKF	908
	*.	

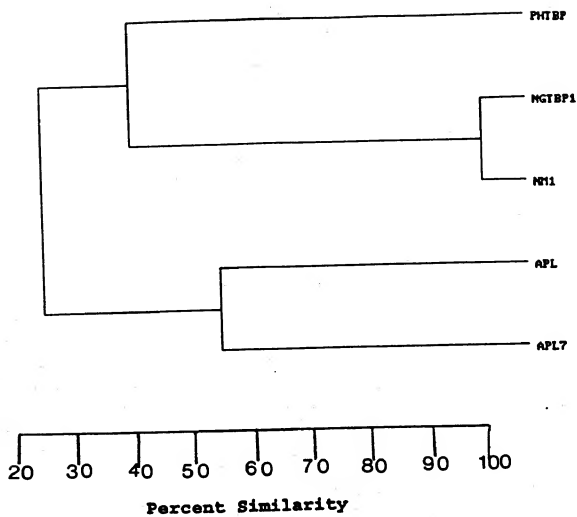
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FIGURE 10

PHTBP1	MIMKYHFRYSTVALTVLFAISHSYGAATENKKIENNDLAVLDEVIVTE	50
APL	MHPKLMFY---ALAFITSLFLVACSGGKSPD-----LEOVPRNQ	36
APL7	MHPKLMFY---ALAFITSLFLVACSGGKSPD-----LEOVPRNQ	36
	
PHTBP1	SHYAHQRQNEVTGLGVVKNYHMSK--NQILG--IRDLTRYDPGISVVE	96
APL	TAKAKATTSYQDRETKKTKHELDKLAEPALGYETQILLRNKAKETBTG	86
APL7	TTGVSKER--YKDVETAKKKEKBLGELKAPALGTVVKV-----FVSSPE	78
	
PHTBP1	QCRGASSGYAIRGVQDKNRVSLLDVGLPQANSYHTLSGDANGAINRI-EY	145
APL	EKRNER-----VVLSEDKITKLYQBSVEIIPB--LDRLNGKTTSDNVYHS	130
APL7	NKK-----VDISD-----IEVITNGNLDOVPYKANSKK-YNY	109
	
PHTBP1	ENIRSIELSGASSABYGGSGAHOAIGPRTKDAQ-DIIEKB	185
APL	HDSKILDKNRDLKYVRSGYVYDGSFNEIRNDSGFHVFKQIDGYVYVYLG	180
APL7	FDIK--TKDSSLQYVRSGYVIDGHEHSGSNEK-----GYVYVYK	145
	
PHTBP1	---QHGLSDKTSYASKNSHPLQIAAAGEAQQFALVIATERN	225
APL	VTPSKELPKGVKIVSYGTWDFVSNINLERSIDGPDTSQDGKXVSAITSITE	230
APL7	NSPAKELPVNQLLTYTGSWDFTSNALANE-----BGRFNTLNDYYTK	189
	
PHTBP1	---GKETKI--HSEANKLONIRRTGCFERNYDFTQIPHRMPPGGSFFIVED	272
APL	TVNRDHKVQEKLGDNVEVKVAHSSSEPAVDPNKLLTGSLYRMG--YINRN	278
APL7	FIGK--RVGLVSGDAKPAKHYKTSQFVDFATKQMTGKL-----SD	228
	
PHTBP1	TCPTLDCTPRARVKLRNDNFVVTFFPHTPEERNABQIPYRTEQ--LSAQ	320
APL	KAEVTKRYSIBADIAGNRFRG--KAKAKAGDPIFT--DSNYLBOG	321
APL7	KEKTI---YTVNADIRGNRPTGAATASDKNGKESYNFYSADSSQSLWG	275
	
PHTBP1	EKTKDRIAPNPLDYKSNVFMKPGYHFNSSHYLGAILEDTKQRTISVIC	370
APL	FYGPFAEBMAGKFFTNKLSLFAVFAAKSENGHTTTERIIDATKIDLTQFN	371
APL7	FYGPFAEBMAGKJVANDKLSLFAVFAAKSENGSNVHTVRIIDASKIDLTNFS	325
	
PHTBP1	KRQLTI---QKTILTYHLGTMPKGIIPMLSVQAKDPLWVAIBPCEVDER	418
APL	AKELNNFGDASVLIIDGQKIDLAGVNFNSKTVEINGKTMVAVACCNSLE	421
APL7	ISELANFGDASVLIIDGKKIKLAGSGFTNKRTIEINGKTMVAVACCNSLE	375
	
PHTBP1	HKRRLGFTYKYKPEKNRWLDSINSCVRLRSRCCALSQODIELY	463
APL	YMK---FQGLWQKQKQGVKDNLSFLQGERATIDRMPAGGNKYKVTWD	467
APL7	YMK---FQGLWQKQKQKPENNLSFLQGERATIDRMPAGGNKYKVTWD	421
	
PHTBP1	---SRHLRLCSOYPVVDNKGQPTLDKSNMYRTERNYQEKATCHSPCI	510
APL	ALVSKGTNMIAEADNNKRESQYKTEFDVNFSDKKVNGKLPDKGVNVVFTV	517
APL7	AQVSKERNVWATADDCKJAGYRTEFDVDFGNKHLGKLPDKGVNVVFTV	471
	
PHTBP1	LKALNAGQGVFKQTKHLNLGLGFESNLIRLTIIGIILFNPIKAGYSYRG	560
APL	DATIN--GNGFIGSAKTSDSGFALDAGSSQKGNVAFSDIKVNGPYGP--T	564
APL7	DAKID--GNGFTGAKTSDBGFALDSSGSSRYENKVPADVAVSGPYGP--T	518
	
PHTBP1	RGRLDNPHYIYRRDPRIETVSLCNTRATLILLRVNKGIRLLLR	604
APL	AGELGGQPHKKSNGSGVAV-----FGAKRQIE--K	593
APL7	AALGGQPHKKSNGSGVAV-----FGAKQGVK--K	547
	

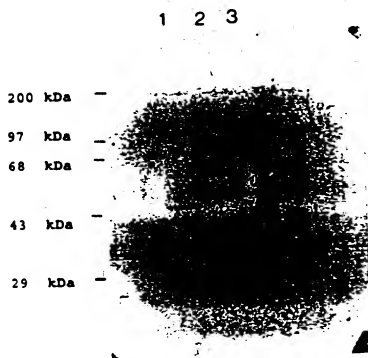
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FIGURE 11



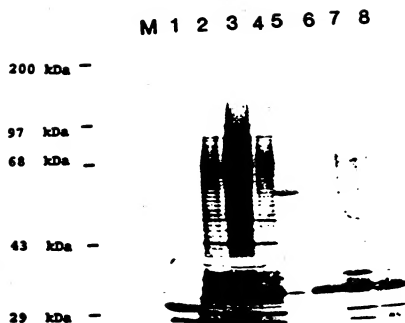
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FIGURE 13



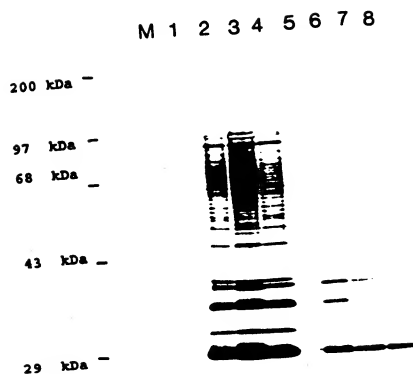
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FIGURE 14



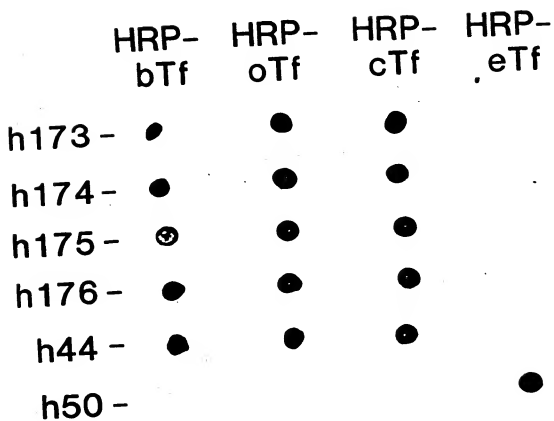
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FIGURE 15



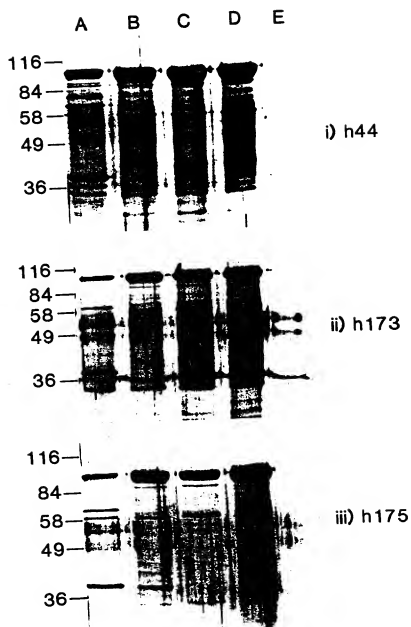
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FIGURE 16



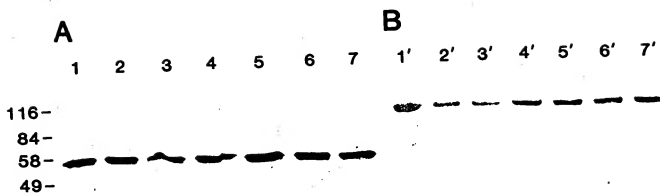
08753750.112096

FIGURE 17



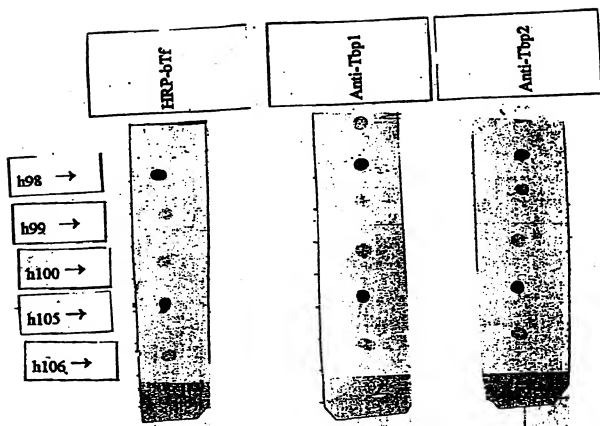
08753750.112996

FIGURE 18



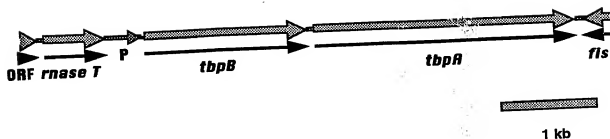
08753750.112996

FIGURE 19



08753750.112996

FIGURE 20



1168
 ATTTTATCTAATCTAAAAACAAGCGTTTCCACCTTGGAATGATTAACATGATC
 CTGAAACTAATAAAGTTCAAACCTTTACATTAAAGTTTATATTATAAATTATAATGA
 -35 -10
 TTATTATTTTATAAAATTAAAGGAGACATTATGTTTAAACTTAAAGTAGTTTGTGA
 SD Met₁₃₀₉
 CTG.....*tbpB*.....GAAAAATAATCATAATTCCTTTGCTGGTTGTAG
 SC₃₀₆₃
 ATAGCAAGCGGGCAATTTTATATAAAATTTGC AAAATTTAAATAAGGAGACCCCT
 SD
 ATCTAATGATAATGAAATATCATCATTTTCGC.....*tbpA*.....AGAAA
 Met₃₁₅₁
 TTTCAGTTTAGCATTTGAAATGAAGTTT TAG.
 SC₅₉₄₃

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FIGURE 23

ATGTTTAAACTTAAAAGTAGTTTTGTACTGCTTAATGCGGCGCTACTTGCCTGCTTGTTCCT
CAAATGGTGGAAAGCTTTGATGTTCAATCTGCCAAAGTTGAATCTCAAACGCAAACTACCCC
CAAAAAGCCCAAGTTTACAAGATGATAATAGTAACGCAAGACGTACAGTAAGCGCTTCTGAA
ACTGAAGCTTTATTGTCAGCCGGGGTTTTGGTTTTTCAGCCAAAATTCGCGCTCGTAATCTCC
TTCCGCAAGGGAAGGAAGATGTAGCCCCATTTGGTGATATAAAAGAGATTACTGGAGATCT
GCCAAAAATTCCGTATGAAGAAGAGGTTAAAGCGTGCGGTAGTAGTGCTGATGGATTTAGC
CATACTCATGATAGAAAATCATAAGTTGTATACAGAGATTTTAAATTTTGTTCGTTCCGGCT
ATGTGTGTGCTTCTGGTCCAAAACCTGAAATAAAGCCTTAAAGAAATTTTGAGAACAGGTGC
ACATGGGTATGTTTTACTATTTAGGTATAGAGCCGCCCAAAGCAATACCTACCCAAAACTA
ACTTTATAAAGGATATTGGGATTTTACTACCTATGCGGCTAAGGGGAGAGATAGTAATATT
TTCATAATCCCGCAGGCATCAATAGTGGCGCCATACCGGAAAATAGTCACGATATTAATGT
TGATGATTCTGAAAAACCAATGGGCATACAGGAGAAATTCAGGCTGATTTTGTCTAATAAA
ACTTTAACTGGAACTTTGGTTTCGTAAATGGGTATGTTAGTCGTAGCAAAGAGCAAAAAATTA
CAACAATTTACGATATTGATGCGAAAAATTAAGGTAAATCGCTTTTCTGGTAAAGCAAAACC
AAAAAAACCGATGATCCTTTATTTTGGGAAAAGCTCCACGACACTTGAAGGTGGATTTTTT
GGTGGGGAGGCTCAAGAACTTGCCGGTAAATTTCTAGCTGATGATAAGTCGGTATTTGTGTG
TTTTTGTCTGGCACACGAGATGCTAAAAAAGATGATAGTGAATCTGCCTTTGATGCTTTCCC
AATTTAACTTAAAGATTTTAAATAAATCTGAGATGGATACTTTCGGGAATCGGACACATTTG
ATTATTAACAATAAGCAGATTCCACTTATTTGCGGAAGCCCAAAAAGCTTTGCGCGAGATGA
AATTTGATGATTGGTTACCCGTACTATTGATGGAAGGAAATTAATAGTGATCTGCTG
TAATAATTTAGATTATGTCAAAATTTGGGATTTATAGCGAGGGAAATAATAGTGATCTGCT
CTCCAAGAAATTTAGTAGGAGAACGTACAGCTCTGGCAGATTGGCAACAGGGACAGTAA
AATATCGAGGTACTTGGGACGGGGTAAATGTACAGTAAATCTGGCTCGGCAGGGGTTGAATC
GCCAAGTAACAGCGAAAGTGGTACTCGTTCACTATTTCGATGTAGATTTTGTCAATAAAAAA
ATTAATGGCAAGCTGATTGCTAATGATGGTGTGAAGAACGCCAAATGCTGACACTGGAAG
GCAATCTGAAAAGGAATGGTTTTGGAGGCACAGCCAAAACGGGCAATCTCGTTTAAATCT
TGATCCCAAAAGTACGAATGGTGGCAGGTTAGGTCATATAAATACTCAATTTGAAGGGGC
TTTTATGGCCCTAAGGCGACGGAATTAGGTGGTATTGTACAAAATACAGAAACGGATAAAG
ATAGAGTCAGTATTACATTCCGGCGAAAACGTCAAATAGAAAAATAA

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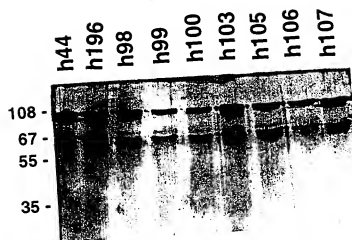
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FIGURE 25

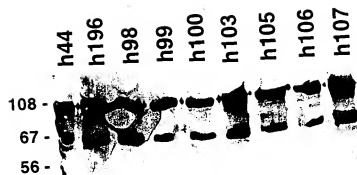
	HRP-bTf	HRP-oTf	HRP-gTf
h44 Fe +			
h44 Fe -			
h196			
h98			
h99			
h100			
h103			
h105			
h106			
h107			

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FIGURE 26



A



B

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FIGURE 27

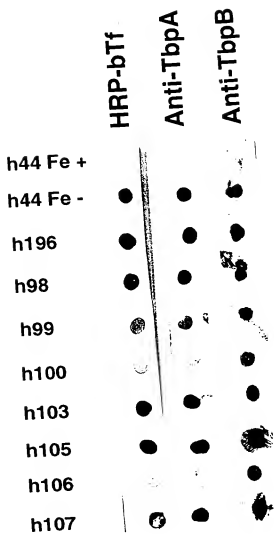
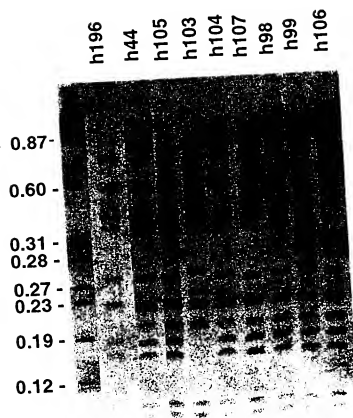
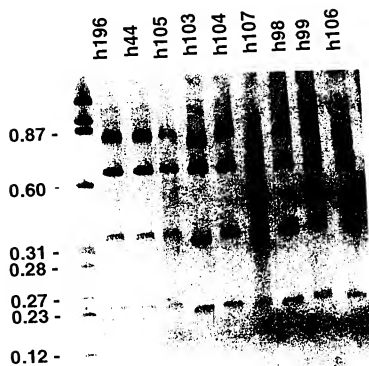


FIGURE 28



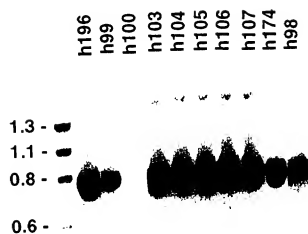
A



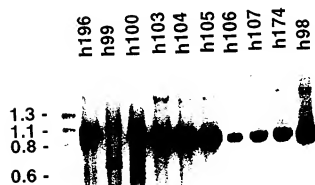
B

966211-05/ES/80

FIGURE 29



A



B

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